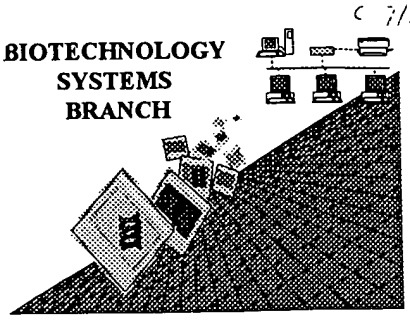
RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/203,768

Art Unit / Team No. : 1816

Date Processed by STIC: 12/9/98

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

This Raw Listing contains the General Information Section and up to first 5 pages.

MANDATORY numeric identifier and response needed
mandatory numeric identifier and response needed if filed before assignment of serial number
MANDATORY numeric identifier and response needed (8 shown)
New format

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W--> 3 <130>
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5 <141> 1998-12-02
E--> 6 <160>
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8 <211> 417
9 <212> DNA
10 <213> Homo sapiens
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12 <221> CDS
13 <222> (1)..(417)
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15 <221> sig_peptide
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20          1               5                  10                  15
21        gtc ctg tcc cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag   96
22        Val Leu Ser Gln Val Gln Leu Gln Gln Trp Gly Ala Gly Leu Leu Lys
23                    20                  25                  30
24        cct tcg gag acc ctg tcc ctc acc tgc gct gtc tat ggt ggg tcc ttc   144
25        Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
26                35                  40                  45
27        agt ggt tac tac tgg agc tgg atc cgc cag ccc cca ggg aag ggg ctg   192
28        Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
29             50                  55                  60
30        gag tgg att ggg gaa atc aat cat agt gga agc acc aac tac aac ccg   240
31        Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
32         65                  70                  75                  80
33        tcc ctc aag agt cga gtc acc ata tca gta gac acg tcc aag aac cag   288
34        Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
35                        85                  90                  95
36        ttc tcc ctg aag ctg agc tct gtg acc gcc gcg gac acg gct gtg tat   336
37        Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
38                    100                 105                 110
39        tac tgt gcg aga gaa ata gca gct cgt cct cac cga tac ttt gac tac   384
40        Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
41                115                 120                 125
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44            130                 135
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             20                  25                  30
Pro Ser Glu Thr Leu Ser Leu Thr Cys Ala Val Tyr Gly Gly Ser Phe
         35                  40                  45
Ser Gly Tyr Tyr Trp Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu
     50                  55                  60
Glu Trp Ile Gly Glu Ile Asn His Ser Gly Ser Thr Asn Tyr Asn Pro
 65                  70                  75                  80
Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser Lys Asn Gln
                 85                  90                  95
Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr
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Tyr Cys Ala Arg Glu Ile Ala Ala Arg Pro His Arg Tyr Phe Asp Tyr
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Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctc tcc tgc agg   96
Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg
             20                  25                  30
gcc agt cag agt gtt agc agc aac tta gcc tgg tac cag cag aaa cct   144
Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
         35                  40                  45
ggc cag gct ccc agg ctc ctc atc tat ggt gca tcc acc agg gcc act   192
Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
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Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
 65                  70                  75                  80
ctc acc atc agc agc ctg cag tct gaa gat ttt gca gtt tat tac tgt   288
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 96                          85                  90                  95
 97          cag cag tat aat aac tgg cct ccg tac act ttt ggc cag ggg acc aag   336
 98          Gln Gln Tyr Asn Asn Trp Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
 99                      100                 105                 110
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112          Ala Ser Gln Ser Val Ser Ser Asn Leu Ala Trp Tyr Gln Gln Lys Pro
113                   35                  40                  45
114          Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr
115               50                  55                  60
116          Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
117           65                  70                  75                  80
118          Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys
119                          85                  90                  95
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134            1               5                  10                  15
135          tcg gtg aag gtc tcc tgc aag gct tct gga ggc acc ttc agc agc tat   96
136          Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
137                       20                  25                  30
138          gct atc agc tgg gtg cga cag gcc cct gga caa ggg ctt gag tgg atg   144
139          Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
140                   35                  40                  45
141          gga ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc   192
142          Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
143               50                  55                  60
144          cag ggc aga gtc acg att acc gcg gac gaa tcc acg agc aca gcc tac   240
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145         Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
146          65                  70                  75                  80
147         atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac tgt   288
148         Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
149                         85                  90                  95
150         gcg aga gaa gat agc agt ggc tgg tat cac tac tgg ggc cag gga acc   336
151         Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
152                     100                 105                 110
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159   <213> Homo sapiens
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163         Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
164                      20                  25                  30
165         Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
166                  35                  40                  45
167         Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
168              50                  55                  60
169         Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
170          65                  70                  75                  80
171         Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
172                         85                  90                  95
173         Ala Arg Glu Asp Ser Ser Gly Trp Tyr His Tyr Trp Gly Gln Gly Thr
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187           1               5                  10                  15
188         aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca   96
189         Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala
190                      20                  25                  30
191         agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat   144
192         Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr
193                  35                  40                  45
194         ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc   192
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195          Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser
196               50                  55                  60
197          agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa   240
198          Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu
199           65                  70                  75                  80
200          gat gag gct gac tat tac tgt aac tcc cgg gac agc agt ggt aac ccc   288
201          Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Ser Ser Gly Asn Pro
202                          85                  90                  95
203          gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta ggt cag ccc       333
204          Val Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro
205                      100                 105                 110
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VERIFICATION SUMMARY
PATENT APPLICATION **US/09/203,768**

Input Set: **I203768.RAW**

Line	?	Error/Warning	Original Text
1	E	Response to "Applicant" Name is Missing	
2	E	Response to "Title of Invention" Missing	
3	W	Response to "File Reference" is Missing	
6	E	# of Seq. 0 Not Equal Actual 8	